OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/964,678A

DATE: 02/06/2002
TIME: 11:39:29

Input Set : A:\seqlist 0609_4370002 ascii
Output Set: N:\CRF3\02062002\I964678A.raw

p.5

ENTERED

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 5 <110> APPLICANT: de la Monte, Suzanne
 7       Wands, Jack R.
11 <120> TITLE OF INVENTION: Transgenic Animals and Cell Lines for Screening Drugs
12       Effective for the Treatment or Prevention of
13       Alzheimer's Disease
17 <130> FILE REFERENCE: 0609.4370002
21 <140> CURRENT APPLICATION NUMBER: 09/964,678A
23 <141> CURRENT FILING DATE: 2001-09-28
27 <150> PRIOR APPLICATION NUMBER: 09/380,203
29 <151> PRIOR FILING DATE: 2000-04-25
33 <150> PRIOR APPLICATION NUMBER: PCT/US98/03685
35 <151> PRIOR FILING DATE: 1998-02-26
39 <150> PRIOR APPLICATION NUMBER: 60/038,908
41 <151> PRIOR FILING DATE: 1997-02-26
45 <160> NUMBER OF SEQ ID NOS: 14
49 <170> SOFTWARE: PatentIn version 3.1
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55 <211> LENGTH: 1442
57 <212> TYPE: DNA
59 <213> ORGANISM: Unknown
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65 <223> OTHER INFORMATION: AD7c-NTP cDNA
67 <220> FEATURE:
69 <221> NAME/KEY: CDS
71 <222> LOCATION: (15)..(1139)
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82 aat ggc gca atc tca gct cac cgc aac ctc cgc ctc ccg ggt tca agc        98
83 Asn Gly Ala Ile Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser
84            15                  20                  25
86 gat tct cct gcc tca gcc tcc cca gta gct ggg att aca ggc atg tgc       146
87 Asp Ser Pro Ala Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys
88        30                  35                  40
90 acc cac gct cgg cta att ttg tat ttt ttt tta gta gag atg gag ttt       194
91 Thr His Ala Arg Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe
92 45                  50                  55                  60
94 ctc cat gtt ggt cag gct ggt ctc gaa ctc ccg acc tca gat gat ccc       242
95 Leu His Val Gly Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro
96                65                  70                  75
98 tcc gtc tcg gcc tcc caa agt gct aga tac agg act ggc cac cat gcc       290
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99 Ser Val Ser Ala Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala
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102 cgg ctc tgc ctg gct aat ttt tgt ggt aga aac agg gtt tca ctg atg      338
103 Arg Leu Cys Leu Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met
104         95                  100                 105
106 tgc cca agc tgg tct cct gag ctc aag cag tcc acc tgc ctc agc ctc      386
107 Cys Pro Ser Trp Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu
108     110                 115                 120
110 cca aag tgc tgg gat tac agg cgt gca gcc gtg cct ggc ctt ttt att      434
111 Pro Lys Cys Trp Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile
112 125                 130                 135                 140
114 tta ttt ttt tta aga cac agg tgt ccc act ctt acc cag gat gaa gtg      482
115 Leu Phe Phe Leu Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val
116                 145                 150                 155
118 cag tgg tgt gat cac agc tca ctg cag cct tca act cct gag atc aag      530
119 Gln Trp Cys Asp His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys
120             160                 165                 170
122 cat cct cct gcc tca gcc tcc caa gta gct ggg acc aaa gac atg cac      578
123 His Pro Pro Ala Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His
124         175                 180                 185
126 cac tac acc tgg cta att ttt att ttt att ttt aat ttt ttg aga cag      626
127 His Tyr Thr Trp Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln
128     190                 195                 200
130 agt ctc aac tct gtc acc cag gct gga gtg cag tgg cgc aat ctt ggc      674
131 Ser Leu Asn Ser Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly
132 205                 210                 215                 220
134 tca ctg caa cct ctg cct ccc ggg ttc aag tta ttc tcc tgc ccc agc      722
135 Ser Leu Gln Pro Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser
136                 225                 230                 235
138 ctc ctg agt agc tgg gac tac agg cgc cca cca cgc cta gct aat ttt      770
139 Leu Leu Ser Ser Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe
140             240                 245                 250
142 ttt gta ttt tta gta gag atg ggg ttc acc atg ttc gcc agg ttg atc      818
143 Phe Val Phe Leu Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile
144         255                 260                 265
146 ttg atc tct gga cct tgt gat ctg cct gcc tcg gcc tcc caa agt gct      866
147 Leu Ile Ser Gly Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala
148     270                 275                 280
150 ggg att aca ggc gtg agc cac cac gcc cgg ctt att ttt aat ttt tgt      914
151 Gly Ile Thr Gly Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys
152 285                 290                 295                 300
154 ttg ttt gaa atg gaa tct cac tct gtt acc cag gct gga gtg caa tgg      962
155 Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp
156                 305                 310                 315
158 cca aat ctc ggc tca ctg caa cct ctg cct ccc ggg ctc aag cga ttc     1010
159 Pro Asn Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe
160             320                 325                 330
162 tcc tgt ctc agc ctc cca agc agc tgg gat tac ggg cac ctg cca cca     1058
163 Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro
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164         335                 340                 345          1106
166 cac ccc gct aat ttt tgt att ttc att aga ggc ggg gtt tca cca tat
167 His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr
168     350                 355                 360              1159
170 ttg tca ggc tgg tct caa act cct gac ctc agg tgacccacct gcctcagcct
171 Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg
172 365                 370                 375
174 tccaaagtgc tgggattaca ggcgtgagcc acctcaccca gccggctaat ttagataaaa  1219
176 aaatatgtag caatgggggg tcttgctatg ttgcccaggc tggtctcaaa cttctggctt  1279
178 catgcaatcc ttccaaatga gccacaacac ccagccagtc acatttttta aacagttaca  1339
180 tctttatttt agtatactag aaagtaatac aataaacatg tcaaacctgc aaattcagta  1399
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187 <211> LENGTH: 375
189 <212> TYPE: PRT
191 <213> ORGANISM: Unknown
195 <220> FEATURE:
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206             20                  25                  30
209 Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys Thr His Ala Arg
210         35                  40                  45
213 Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly
214     50                  55                  60
217 Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro Ser Val Ser Ala
218 65                  70                  75                  80
221 Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Cys Leu
222                 85                  90                  95
225 Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met Cys Pro Ser Trp
226             100                 105                 110
229 Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu Pro Lys Cys Trp
230         115                 120                 125
233 Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile Leu Phe Phe Leu
234     130                 135                 140
237 Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val Gln Trp Cys Asp
238 145                 150                 155                 160
241 His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys His Pro Pro Ala
242                 165                 170                 175
245 Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His His Tyr Thr Trp
246             180                 185                 190
249 Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln Ser Leu Asn Ser
250         195                 200                 205
253 Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly Ser Leu Gln Pro
254     210                 215                 220
257 Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser Leu Leu Ser Ser
258 225                 230                 235                 240
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261 Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe Phe Val Phe Leu
262                 245                 250                 255
265 Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile Leu Ile Ser Gly
266             260                 265                 270
269 Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly
270         275                 280                 285
273 Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys Leu Phe Glu Met
274     290                 295                 300
277 Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp Pro Asn Leu Gly
278 305                 310                 315                 320
281 Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe Ser Cys Leu Ser
282                 325                 330                 335
285 Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro His Pro Ala Asn
286             340                 345                 350
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290         355                 360                 365
293 Ser Gln Thr Pro Asp Leu Arg
294     370                 375
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301 <212> TYPE: DNA
303 <213> ORGANISM: Unknown
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309 <223> OTHER INFORMATION: Incorrect sequence of AD7c-NTP DNA
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314 ctcagctcac cgcaacctcc gcctcccggg ttcaagcgat tctcctgcct cagcctcccc    120
316 agtagctggg attacaggca tgtgcaccac gctcggctaa ttttgtattt ttttttagta    180
318 gagatggagt ttaactccat gttggtcagg ctggtctcga actcccgacc tcagatgatc    240
320 tcccgtctcg gcctgcccaa agtgctgaga ttacaggcat gagccaccat gcccggcctc    300
322 tgcctggcta atttttgtgg tagaaacagg gtttcactga tgttgcccaa gctggtctcc    360
324 tgagctcaag cagtccacct gcctcagcct cccaaagtgc tgggattaca ggcgtcagcc    420
326 gtgcctggcc ttttttatttt atttttttta agacacaggt gtaccactct tacccaggat    480
328 gaagtgcagt ggtgtgatca cagctcactg cagccttcaa ctcctgagat caagcaatcc    540
330 tcctgcctca gcctcccaag tagctgggac caaagacatg caccactaca cctggtaatt    600
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334 agtggcgcaa tcttggctca ctgcaacctc tgcctcccgg gttcaagtta ttctcctgcc    720
336 ccagcctcct gagtagctgg gactacaggc gcccaccacg cctagctaat ttttttgtat    780
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340 gatctgcctg cctcggccta cccaaagtgc tgggattaca ggtcgtgact ccacgccggc    900
342 ctatttttaa tttttgtttg tttgaaatgg aatctcactc tgttacccag gtcggagtgc    960
344 aatggcaaat ctcggctact cgcaacctct gcctcccggg tcaagcgatt ctcctgtctc   1020
346 agcctcccaa gcagctggga ttacgggacc tgcaccacac cccgctaatt tttgtatttt   1080
348 cattagaggc gggtttacca tatttgtcag gctgggtctc aaactcctga cctcaggtga   1140
350 cccacctgcc tcagccttcc aaagtgctgg gattacaggc gtgagccacc tcacccagcc   1200
352 ggctaatttg gaataaaaaa tatgtagcaa tgggggtctg ctatgttgcc caggctggtc   1260
354 tcaaacttct ggcttcagtc aatccttcca aatgagccac aacacccagc cagtcacatt   1320
356 ttttaaacag ttacatcttt attttagtat actagaaagt aatacaataa acatgtcaaa   1380
358 c                                                                  1381
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DATE: 02/06/2002
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Input Set : A:\seqlist 0609_4370002 ascii
Output Set: N:\CRF3\02062002\I964678A.raw

361 <210> SEQ ID NO: 4
363 <211> LENGTH: 1418
365 <212> TYPE: DNA
367 <213> ORGANISM: Unknown
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375 <400> SEQUENCE: 4
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380 agtaggctgg gattacaggc atgtgcacca cgctcggcta attttgtatt ttttttagt 180
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384 cccgtctcgg cctcccaaag tgctagatac aggactgagc accatgcccg gcctctgcct 300
386 ggctaatttt tgtggtagaa acagggtttc actgatgtgc ccaagctggt ctcctgagct 360
388 caagcagtcc acctgcctca gcctcccaaa gtgctgggat tacaggcgtg cagccgtgcc 420
390 tggccttttt attttatttt ttttaagaca caggtgtccc actcttaccc aggatgaagt 480
392 gcagtggtgt gatcacagct cactgcagcc ttcaactctg agatcaagca tcctcctgcc 540
394 tcagcctccc aaagtagctg ggaccaaaga catgcaccac tacacctggc taatttttat 600
396 ttttatttt aatttttga gacagagtct caactctgtc acccaggctg gagtgcagtg 660
398 gcgcaatctt ggctcactgc aacctctgcc tcccgggttc aagttattct cctgccccag 720
400 cctcctgagt agctgggact acaggcgccc accacgccta gctaattttt ttgtattttt 780
402 agtagagatg gggtttcacc atgttcgcca ggttgatgct agatctcttg accttgtgat 840
404 ctgcctgcct cggcctccca aagtgctggg attacaggac gtgacgccca ccgcccggcc 900
406 tatttttaat ttttgtttgt ttgaaatgga atctcactct gttacccagg ctggagtgca 960
408 atggccaaat ctcggctcac tgcaacctct gcctcccggg ctcaagcgat tctcctgtct 1020
410 cagcctccca agcagctggg attacgggca cctgcaccac accccgctaa tttttgtatt 1080
412 ttcattagag gcggggtttc accatatttg tcaggctggt ctcaaactcc tgacctcagg 1140
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416 cggctaattt agataaaaaa atatgtagca atgggggtc ttgctatgtt gcccaggctg 1260
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427 <211> LENGTH: 22
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431 <213> ORGANISM: Artificial Sequence
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437 <223> OTHER INFORMATION: AD7c-NTP oligonucleotide
439 <400> SEQUENCE: 5
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443 <210> SEQ ID NO: 6
445 <211> LENGTH: 24
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449 <213> ORGANISM: Artificial Sequence
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457 <400> SEQUENCE: 6
458 aagcaggcag atcacaaggt ccag 24
461 <210> SEQ ID NO: 7
463 <211> LENGTH: 20

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

2/6/02

VERIFICATION SUMMARY DATE: 02/06/2002
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L:604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:632 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14